

337988 acid proteinase light chain - slime mold (Physarum polycephalum) (fragment) RESULT 6
 C;Species: Physarum polycephalum
 C;Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 30-Sep-1993
 C;Accession: B37988
 R;Murakami-Murofushi, K.; Takahashi, T.; Minowa, Y.; Iino, S.; Takeuchi, T.; Kitagaki, Og
 J;Biol. Chem. 265, 1989-19903, 1990
 A;Title: Purification and characterization of a novel intracellular acid proteinase from
 A;Reference number: A337988; MUID:91060608; PMID:22465666
 A;Accession: B37988
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-5 <MOR>
 A;Molecule type: protein
 A;Residues: 1-7 <MOR>
 C;Comment: The biological activity of this peptide was not determined.
 C;Species: Phyllomeida rohdei (Rohde's leaf frog)
 C;Accession: A61081
 C;Species: Phyllomeida rohdei (Rohde's leaf frog)
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Aug-2000
 C;Superfamily: unassigned animal peptides
 C;Keywords: amidated carboxyl end; hydroxyproline; skin
 F;3' Modified site: 4-hydroxyproline (Pro) #status experimental
 F;7' Modified site: amidated carboxyl end (Pro) #status experimental
 A;Accession number: A61081
 A;Reference number: A61081
 A;Accession: A61081
 A;Molecule type: protein
 A;Residues: 1-7 <MOR>
 C;Comment: The biological activity of this peptide was not determined.
 C;Species: unassigned animal peptides
 C;Superfamily: unassigned animal peptides
 C;Keywords: amidated carboxyl end; hydroxyproline; skin
 F;3' Modified site: 4-hydroxyproline (Pro) #status experimental
 F;7' Modified site: amidated carboxyl end (Pro) #status experimental
 Query Match Score 16; DB 2; Length 5;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 QPP 3
 Db 2 EPP 4
 Qy 1 QPPR 4
 Db 4 QPQR 7
 RESULT 4
 B324749 neuropeptide B - bovine
 C;Species: Bos primigenius taurinus (cattle)
 C;Accession: B24749
 R;Yang, H.Y.T.; Fratta, W.; Majane, E.A.; Costa, E.
 Proc. Natl. Acad. Sci. U.S.A. 82, 7757-7761, 1995
 A;Title: Isolation, sequencing, synthesis, and pharmacological characterization of two b
 A;Reference number: A94074; MUID:86067985; PMID:3865193
 A;Accession: B24749
 A;Molecule type: protein
 A;Residues: 1-8 <YAN>
 C;Superfamily: unassigned animal peptides
 C;Keywords: neuropeptide
 Query Match Score 16; DB 2; Length 8;
 Best Local Similarity 75.0%; Pred. No. 2.2e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 QPPR 4
 Db 4 QPQR 7
 RESULT 5
 B32945 endoglycosylceramidase (EC 3.2.1.123) I - Rhodococcus sp. (fragment)
 C;Species: Rhodococcus sp.
 C;Accession: B32945
 R;Ito, M.; Iregami, Y.; Yamagata, T.
 J. Biol. Chem. 266, 7919-7926, 1991
 A;Title: Activator proteins for glycosphingolipid hydrolysis by endoglycosylceramidases. I
 A;Reference number: A33945; MUID:91210321; PMID:1850427
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-8 <ITC>
 C;Keywords: Glycosidase; hydrolase
 Query Match Score 16; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.4e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 PRA 5
 Db 6 PRA 8
 RESULT 6
 A61081 tryptophyllin, basic - Rohde's leaf frog
 C;Species: Phyllomeida rohdei (Rohde's leaf frog)
 C;Accession: A61081
 R;Montecuccchi, P.C.; Vincenti, M.; Lazzarini, A.M.; Rusconi, L.; Espanier, V.
 Int. J. Pept. Protein Res. 33, 391-395, 1989
 A;Title: Isolation, structure determination and synthesis of a novel tryptophan-contains
 A;Reference number: A61081
 A;Accession: A61081
 A;Molecule type: protein
 A;Residues: 1-7 <MOR>
 C;Comment: The biological activity of this peptide was not determined.
 C;Species: unassigned animal peptides
 C;Superfamily: unassigned animal peptides
 C;Keywords: amidated carboxyl end; hydroxyproline; skin
 F;3' Modified site: 4-hydroxyproline (Pro) #status experimental
 F;7' Modified site: amidated carboxyl end (Pro) #status experimental
 Query Match Score 15; DB 2; Length 7;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 QPP 3
 Db 1 KPP 3
 RESULT 7
 A339690 neural cell adhesion molecule, cardiac splice form, -,-,-,- rat (fragment)
 C;Species: Rattus norvegicus (Norway rat)
 C;Accession: A339690
 C;Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mRN
 A;Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mRN
 A;Reference number: A339690; MUID:9114516; PMID:199615
 A;Accession: A339690
 A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
 A;Molecule type: mRNA
 A;Residues: 1-7 <REV>
 A;Cross-references: GB:M63970
 C;Keywords: cardiac muscle; cell adhesion; heart
 Query Match Score 15; DB 2; Length 7;
 Best Local Similarity 75.0%; Pred. No. 2.3e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 QPPR 4
 Db 1 QPVR 4
 RESULT 8
 S15597 orf 4 rare 5'-region - human
 C;Species: Homo sapiens (man)
 C;Accession: S15597
 R;Brand, N.J.; Petrovich, M.; Chambon, P.
 Nuclic Acids Res. 18, 6799-6806, 1990
 A;Title: Characterization of a functional promoter for the human retinoic acid receptor-
 A;Reference number: S15594; MUID:91088249; PMID:2173878
 A;Accession: S15597
 A;Molecule type: DNA
 A;Residues: 1-7 <BBA>
 A;Cross-references: EMBL:X56058; NID:935876
 A;Note: this ORF from Fig. 2 is not annotated in GenBank entry HSRARA2, release 111.0
 C;Comment: This sequence is not thought to be translated.
 C;Genetics:
 A;Gene: GDB:RARA

A;Cross-references: GDB:1120337; OMIM:180240
 A;Map position: 17q12-17q12
 Query Match 34.9%; Score 15; DB 4; Length 7;
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 A;Keywords: glycosidase; hydrolase; polysaccharide degradation

Qy 3 PRAAI 7
 Db 2 PRGGV 6

RESULT 9
 S16324 hypothetical protein 2 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 21-Nov-1993 #sequence_revision 12-May-1995 #text_change 21-Jul-2000
 C;Accession: S16324
 R;Roberti, I.; Sessa, G.; Lucchetti, S.; Morelli, G.
 EMBO J 10, 1787-1791, 1991
 A;Title: A novel class of plant proteins containing a homeodomain with a closely linked
 A;Reference number: S16323; MUID:91266307; PMID:1675503
 A;Accession: S16324
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-8 <RUB>
 A;Cross-references: EMBL:X58821; NID:916327; PIDN:CAA41624.1; PID:9579259

Query Match 32.6%; Score 14; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 A;Keywords: protein

Qy 2 PP 3
 Db 7 PP 8

RESULT 10
 S21288 lectin - potato (fragment)
 C;Species: Solanum tuberosum (potato)
 C;Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 05-Dec-1998
 C;Accession: S21288
 R;Millar, D.J.; Allen, A.K.; Smith, C.G.; Sidebottom, C.; Slabas, A.R.; Bolwell, G.P.
 Biochem. J. 283, 813-821, 1992
 A;Title: Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characteristic
 A;Reference number: S21288; MUID:92272683; PMID:1590771
 A;Accession: S21288
 A;Molecule type: protein
 A;Residues: 1-8 <MIL>
 A;Experimental source: var. Ulster Sceptre
 C;Function: may be involved in defence mechanism of the plant
 C;Keywords: hydroxyproline; lectin

Query Match 32.6%; Score 14; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 A;Keywords: protein

Qy 2 PP 3
 Db 7 PP 8

RESULT 11
 PT0030 inulinase (EC 3.2.1.7) - Aspergillus ficium (fragment)
 N;Alternative names: inulase
 C;Species: Aspergillus ficium
 C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 07-May-1999
 C;Accession: PT0030
 R;Ettalibi, M.; Baratti, J.C.
 Agric. Biol. Chem. 54, 61-68, 1990

A;Title: Molecular and kinetic properties of Aspergillus ficium inulinases.
 A;Reference number: PT0030; MUID:90344234; PMID:1368326
 A;Molecule type: protein
 A;Accession: PT0030
 A;Residues: 1-8 <ERT>
 C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 32.6%; Score 14; DB 2; Length 8;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QPPR 4
 Db 5 QPYR 8

RESULT 12
 E47393 neuropeptide callostatin 5 - bluebottle fly (Calliphora vomitoria)
 C;Species: Calliphora vomitoria
 C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 03-Mar-1995
 C;Accession: E47393
 R;Dove, H.; Johnsen, A.H.; Scott, A.G.; Yu, C.G.; Yagi, K.J.; Tobe, S.S.; Thorpe, A.
 Proc. Natl. Acad. Sci. U.S.A. 90, 2456-2460, 1993
 A;Title: Callostatins: neuropeptides from the blowfly Calliphora vomitoria with sequen
 A;Reference number: A47393; MUID:91211980; PMID:8460157
 A;Accession: E47393
 A;Status: preliminary
 A;Molecule type: protein
 A;Accession: 1-8 <DUV>
 A;Experimental source: whole flies
 A;Note: sequence extracted from NCBI backbone (NCBIP:128482)

Query Match 32.6%; Score 14; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PP 3
 Db 2 PP 3

RESULT 13
 S10783 enamelin f - bovine (fragment)
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
 C;Accession: S10783
 R;Itrawich, B.; Glimcher, M.J.
 Eur. J. Biochem. 191, 47-56, 1990
 A;Title: 'Tooth' enamellins, identified mainly as serum proteins. Major 'enamelin' is albu
 A;Reference number: S10780; MUID:2379503
 A;Accession: S10783
 A;Molecule type: protein
 A;Residues: 1-8 <STR>
 C;Keywords: enamel; phosphoprotein

Query Match 32.6%; Score 14; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PP 3
 Db 4 PP 5

RESULT 14
 PT0059 inulin receptor beta chain V-D-J region (126-1BH) - mouse (fragment)
 T-cell receptor beta chain V-D-J region (126-1BH)
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C;Accession: PT0059
 R;Feeney, A.J.

J. EXP. MED. 174, 115-124, 1991
 A; Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A; Reference number: PR0509; MUID:91277601; PMID:1711558
 A; Accession: PR0559
 A; Status: translation not shown
 A; Molecule type: mRNA
 A; Residues: 1-8 <FEE>
 A; Experimental source: day 18 fetal thymus, strain BALB/c
 C; Keywords: T-cell receptor

Query Match 32.6%; Score 14; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 PP 3
 Db 4 PP 5

RESULT 15

S22428
 chitin-binding protein - potato (fragment)
 C; Species: Solanum tuberosum (potato)
 C; Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 05-Dec-1998
 C; Accession: S22428
 R; Millar, D.J.; Allen, A.K.; Smith, C.G.; Sidebottom, C.; Slabas, A.R.; Bobwell, G.P.
 Biochem. J. 283, 813-821, 1992
 A; Title: Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characterization
 A; Reference number: S21288; MUID:9227683; PMID:1590771
 A; Accession: S22428
 A; Molecule type: protein
 A; Residues: 1-8 <PRIL>
 C; Function:
 A; Description: may be involved in plant defense
 C; Keywords: glycoprotein, hydroxyproline

Query Match 30.2%; Score 13; DB 2; Length 8;
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Qy 3 PRAAY 8
 Db 1 PXDMVY 6

Search completed: July 28, 2004, 07:55:22
 Job time : 16 secs

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OM protein - protein search, using sw model

Run on: July 28, 2004, 07:17:39 ; Search time 13 Seconds

(without alignments)
32.043 Million cell updates/sec

Title: SEQ3
Perfect score: 43
Sequence: 1 QPPRAAII 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 158

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.2

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	16	37.2	8	1	NPMB_BOVIN	P15507 bos tauris
2	15	34.9	7	1	TPFY_PACDA	P83455 pachymedusa
3	15	34.9	8	1	UFO4_MOUSE	P3642 mus musculus
4	15	34.9	8	1	PPK2_PERAM	P8692 periplaneta
5	14	32.6	8	1	ALL5_CALVO	P4881 caliphora
6	12	27.9	4	1	TUFT_HUMAN	P01858 homo sapiens
7	12	27.9	7	1	LANC_CARIU	P36160 carinobacter
8	12	27.9	8	1	PART7_ASCSU	P41171 ascaris suum
9	12	27.9	8	1	LMT2_LOMCI	P2396 locusta migratoria
10	12	27.9	8	1	LPK_LEUMA	P1049 leucophaea
11	12	27.9	8	1	PPK3_PERAM	P8618 periplaneta
12	12	27.9	8	1	RS7_TWICIT	P3564 mycobacterium
13	12	27.9	8	1	UC26_MAIZE	P0632 zea mays (m)
14	12	27.9	8	1	UPA1_HUMAN	P3087 homo sapiens
15	11	25.6	5	1	PSK_DNUCA	P58261 daucus carota
16	11	25.6	7	1	CIA_ENTFA	P1932 enterococcus
17	11	25.6	7	1	E105_LITRU	P0101 litoria rubra
18	11	25.6	7	1	HY7_FIG	P01153 sus scrofa
19	11	25.6	8	1	THYL_BIG	P56575 ratus norvegicus
20	10	23.3	3	1	ANG2_BOTJA	P0151 sus scrofa
21	10	23.3	8	1	ANG2_BOTJA	Q10582 bothrops jaegeri
22	9	20.9	7	1	ALL3_CARMA	P8806 carinoma
23	9	20.9	7	1	ALL4_CARMA	P8807 carinoma
24	9	20.9	7	1	ALL5_CARMA	P8808 carinoma
25	9	20.9	7	1	MNP1_GEPDE	P42984 leptinotarsa
26	9	20.9	7	1	TY51_LITRU	P82065 litoria rubra
27	9	20.9	7	1	UN06_PINPS	P81675 pinus pinaster
28	9	20.9	8	1	ALL6_CYDPO	P82157 cydia pomonella
29	9	20.9	8	1	ALL7_CARMA	P81809 carinoma
30	9	20.9	8	1	ALL8_CARMA	P81811 carinoma
31	9	20.9	8	1	ALL9_CARMA	P81812 carinoma
32	9	20.9	8	1	LOCK8_LBUNUA	P19990 leucophaea
33	9	20.9	8	1	NS3_NYCTU	P81152 mycobacterium

ALIGNMENTS

RESULT 1						
NPMB_BOVIN	ID	NPMB_BOVIN	STANDARD;	PRT;	8 AA.	
AC	P15507;	ID	01-APR-1990 (Rel. 14, Created)	DT	01-APR-1990 (Rel. 14, Last sequence update)	
				DR	10-OCT-2003 (Rel. 42, Last annotation update)	
				DE	Morphine modulating neuropeptide B.	
				OS	Bos taurus (Bovine).	
				OC	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi; Bovidae; Bovinae; Bos.	
				OC		
				OX	NCBI_TaxID:9913;	
				RN	[1]	
				RP	SEQUENCE, AND SYNTHESIS.	
				RC	TISSUE:Brain;	
				RX	MEDLINE=86067985; PubMed=3865193;	
				RA	Yang H.-Y.T., Fratta W., Majane P.A., Costa E.,	
				RT	"Isolation, sequencing, synthesis, and pharmacological characterization of two brain neuropeptides that modulate the action of morphine."	
				RT	Proc. Natl. Acad. Sci. U.S.A. 92:7757-7761 (1995).	
				CC	-!- FUNCTION: Modulates the action of morphine.	
				CC	-!- SUBCELLULAR LOCATION: Secreted.	
				DR	PIR; B24749; B24749.	
				KW	Neuropeptide; Amidation.	
				FT	MOD_RES 8 8	AMIDATION.
				SQ	SEQUENCE 8 AA;	8D41657769C729 CRC64;
					Query Match	37.2%;
					Best Local Similarity	75.0%;
					Matches 3; Conservative 0; Mismatches 0;	Pred. No. 1.4e+05; Indels 0; Gaps 0; Gaps 0;
				QY	1 QPPR 4	
				Db	4 QPR 7	
RESULT 2						
TBFY_PACDA	ID	TBFY_PACDA	STANDARD;	PRT;	7 AA.	
AC	P83455;	AC	P83455;	DT	28-FEB-2003 (Rel. 41, Created)	
				DT	28-FEB-2003 (Rel. 41, Last sequence update)	
				DT	10-OCT-2003 (Rel. 42, Last annotation update)	
				DE	Tryptophyllin-1 (PdT-1).	
				OS	Pachymedusa dacnicolor (Giant mexican leaf frog).	
				OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hyliidae;	
				OC	Phylomedusinae; Pachymedusa.	
				OX	[1]	
				RN	RP	
				RC	SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF TISSUE-Skin secretion;	
				RA	Chen T.-B., Orr D.F., Shaw C.;	

RT "Pachymedusa dacnicolor trypophyllin-1 (PdT-1): structural characterization, pharmacological activity and cloning of precursor cDNA";
 RT Submitted (SEP-2002) to Swiss-Prot.
 CC -!- FUNCTION: Myoactive. Has selective relaxing activity on vascular smooth muscle.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- MASS SPECTROMETRY: MW=899.2; METHOD=MALDI.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:004586; P:negative regulation of smooth muscle contra. . . ; NAS.
 KW Amphibian defense peptide; Amidation; Hydroxylation.
 MOD RES 3
 FT MOD_BES 7
 FT SEQUENCE 7 AA; 794 MW; 772D37DC776350 CRC64;
 SQ

RESULT 3
 UP004_MOUSE STANDARD; PRT; 7 AA.
 AC P38612;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of fibroblasts (P46) (Fragment).
 OS Mus musculus (Mouse).
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Epiblast; PubMed=7523108;
 RX MEDLINE=0009307;
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RT "Separation and sequencing of familiar and novel murine proteins using preparative two-dimensional gel electrophoresis.";
 RL Electrophoresis 15:735-745 (1994).
 CC -!- MISCELLANEOUS: On the 2D-gel the determined PI of this unknown protein is: 5.0, its MW is: 46 kDa.
 FT NON_TER 7
 SQ SEQUENCE 7 AA; 766 MW; 68640AB77632700 CRC64;

Query Match 34.9%; Score 15; DB 1; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.4e+05; Indels 0; Gaps 0;
 Matches 2; Conservative 1; Mismatches 0; Standard 0;
 Qy 1 QPP 3
 Db 1 KPP 3

RESULT 3
 UP004_MOUSE STANDARD; PRT; 7 AA.
 AC P38612;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of fibroblasts (P46) (Fragment).
 OS Mus musculus (Mouse).
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Epiblast; PubMed=7523108;
 RX MEDLINE=0009307;
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RT "Separation and sequencing of familiar and novel murine proteins using preparative two-dimensional gel electrophoresis.";
 RL Electrophoresis 15:735-745 (1994).
 CC -!- MISCELLANEOUS: On the 2D-gel the determined PI of this unknown protein is: 5.0, its MW is: 46 kDa.
 FT NON_TER 7
 SQ SEQUENCE 7 AA; 766 MW; 68640AB77632700 CRC64;

Query Match 34.9%; Score 15; DB 1; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.4e+05; Indels 0; Gaps 0;
 Matches 2; Conservative 1; Mismatches 0; Standard 0;
 Qy 1 QPP 3
 Db 1 KPP 3

RESULT 4
 PPK2_PERAM STANDARD; PRT; 8 AA.
 AC P82652;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pyrokinin-2 (Pea-PR-2) (EXPPU-amide).
 OS Periplaneta americana (American cockroach).
 OC Neoptera; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Blattidae; Pterygota; Dictyoptera; Blattaria; Blattoidea;
 OC Blattidae; Pterygota; Blattaria; Blattoidea;
 OX NCBI_TaxID=6978;
 RN [1]

RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=9735393; PubMed=9210163;
 RA Predel R., Kellner P., Kaufmann R., Penzlin H., Gaede G.;
 RT "Isolation and structural elucidation of two pyrokinins from the retrocerebral complex of the American cockroach.";
 RT Peptides 18:473-478 (1997).
 RL J. Comp. Neurol. 419:352-363 (2000).
 RN [2]
 TISSUE SPECIFICITY.
 RX MEDLINE=20189894; PubMed=10723010;
 RA Predel R., Eckert N.;
 RT "Tissue-specific distribution of FXPRlamides in the nervous system of the American cockroach.";
 RT J. Comp. Neurol. 419:352-363 (2000).
 CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropism).
 CC -!- TISSUE SPECIFICITY: Corpora cardiaca.
 CC -!- MASS SPECTROMETRY: MW=883; METHOD=MALDI.
 CC -!- SIMILARITY: Belongs to the Pyrokinin family.
 CC -!- MASS SPECTROMETRY: Belongs to the Pyrokinin family.
 DR InterPro; IPR001484; Pyrokinin.
 DR PROSITE; PS00539; PYROTKNIN; FALSE; NEG.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD_FES 8
 SQ SEQUENCE 8 AA; 884 MW; C83416D9D7775 CRC64;

Query Match 34.9%; Score 15; DB 1; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1.4e+05; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Standard 0;
 Qy 2 PPFA 5
 Db 2 PPFA 5

RESULT 5
 ALL5_CALVO STANDARD; PRT; 8 AA.
 AC P41871;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DB Callatostatin 5 (Met-callatostatin 1) (HY23) [Met-callatostatin].
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Calliphora.
 OX NCBI_TaxID=27454;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=3211980; PubMed=8460157;
 RC TISSUE=Head;
 RA Duke H., Johnson A.H., Scott A.G., Tobe S.S., Thorpe A.;
 RA "Callatostatins: neuropeptides from the blowfly Calliphora vomitoria.";
 RT "Callatostatins: neuropeptides from the blowfly Calliphora vomitoria with sequence homology to cockroach allatostatins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460 (1993).
 RN [2]
 RP CHARACTERIZATION, AND HYDROXYLATION.
 RX MEDLINE=94342269; PubMed=8063725;
 RC TISSUE=Head;
 RA Duke H., Johnson A.H., Scott A.G., Tobe S.S., Thorpe A.;
 RA "Callatostatins: neuropeptides from the blowfly Calliphora vomitoria.";
 RT "Callatostatins: neuropeptides from the blowfly Calliphora vomitoria with sequence homology to cockroach allatostatins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460 (1993).
 RN [2]

Query Match 34.9%; Score 15; DB 1; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.4e+05; Indels 0; Gaps 0;
 Matches 2; Conservative 1; Mismatches 0; Standard 0;
 Qy 1 QPP 3
 Db 2 KPP 4

RESULT 4
 PPK2_PERAM STANDARD; PRT; 8 AA.
 AC P82652;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pyrokinin-2 (Pea-PR-2) (EXPPU-amide).
 OS Periplaneta americana (American cockroach).
 OC Neoptera; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Blattidae; Pterygota; Dictyoptera; Blattaria; Blattoidea;
 OC Blattidae; Pterygota; Blattaria; Blattoidea;
 OX NCBI_TaxID=6978;
 RN [1]

FT MOD RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 883 MW; 7D9879CABBA77766 CRC64;
 Query Match 32.6%; Score 14; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PP 3
 DY 2 PP 3
 DB 2 PP 3

RESULT 6
 TUFT_HUMAN STANDARD; PRT; 4 AA.
 AC P01569;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DB Phagocytosis-stimulating peptide (Tuftsin).
 OC Homo sapiens (Human).
 Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=72187087; PubMed=4112769;
 RA Nishioka K., Constantopoulos A., Satch P.S., Najjar V.A.;
 RT "The characteristics, isolation, and synthesis of the phagocytosis
 stimulating peptide tuftsin.";
 RL Biochem. Biophys. Res. Commun. 47:172-179 (1972).
 RN [2]
 RP IMMUNOGLOBULIN CLASS.
 RX MEDLINE=68091045; PubMed=4169272;
 RA Fidalgo B.V., Najjar V.A.;
 RT "The physiological role of the lymphoid system. VI. The stimulatory
 effect of leucophilic gamma globulin (leucokinin) on the phagocytic
 activity of human polymorphonuclear leucocyte.";
 RL Biochemistry 6:3386-3392 (1967).
 CC -!- MISCELLANEOUS: An IgG (called leucokinin) binds reversibly to the
 cell membrane of neutrophils in the blood. Leucokinin on the gamma
 chain releases the active peptide tuftsin from the phagocytic
 Tuftsin is essential for maximum stimulation of the phagocytic
 activity of neutrophils.
 DR PIR: A02147; A02147.
 DR MIM: 191150; -.
 DR GO: GO:003823; F:Antigen binding; NAS.
 DR GO: GO:0006909; P:Phagocytosis; NAS.
 SQ SEQUENCE 4 AA; 501 MW; 74176321C0000000 CRC64;

Query Match 27.9%; Score 12; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 PR 4
 DY 3 PR 4
 DB 3 PR 4

RESULT 7
 ID LANC_CARUI STANDARD; PRT; 7 AA.
 AC P36965;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DB Lantibiotic carriotic carriotic (UT49).
 OS Carnobacterium sp. (strain UT49).
 OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;
 Carnobacterium.
 OX NCBI_TaxID=35782;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=92321768; PubMed=1622206;
 RA Stoffels G., Nissen-Meyer J., Guðmundsdóttir A., Sletten K., Holo H.,
 Nes I.F.;
 RA "Purification and characterization of a new bacteriocin isolated from
 a Carnobacterium sp.,";
 RT Appl. Environ. Microbiol. 58:1417-1422 (1992).
 -!- FUNCTION: Lanthionine-containing peptide antibiotic (lantibiotic).
 CC Active on Gram-positive bacteria.
 KW Antibiotic; Bacteriocin; Lantibiotic.
 FT NON_TSP 7
 SQ SEQUENCE 7 AA; 786 MW; 741776D5B05B810 CRC64;

Query Match 27.9%; Score 12; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QP 2
 DB 5 QP 6

RESULT 8
 FAR7_ASCSU STANDARD; PRT;
 ID FAR7_ASCSU
 AC P43171;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 RL Peptides 16:491-500 (1995).
 CC -!- SIMILARITY: Belongs to the FARP (FMRPamide related peptide)
 family.
 KW Neuropeptide; Amidation.
 FT MODELS 8 AMIDATION;
 SQ SEQUENCE 8 AA; 963 MW; 9CD40059D417687D CRC64;

Query Match 27.9%; Score 12; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PR 4
 DB 3 PR 4

RESULT 9
 ID LM72_LOCMI STANDARD; PRT; 8 AA.
 AC P23366;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DE Locustamotropin 2 (LOM-MT-2).
 OS Locusta migratoria (Migratory Locust).
 OC Bivalvia; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthopteri; Caelifera; Acridomorpha;
 OC Acridoidea; Acriidae;
 OX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Corpora cardiaca.
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
 RT "Isolation, identification and synthesis of locustamotropin II, an

additional neuropeptide of *Locusta migratoria*. Member of the cephalomyoepic peptide family.";

RT Insect Biochem. 20:79-84 (1990).

RL CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic activity).

CC -!- SIMILARITY: Belongs to the pyrokinin family.

DR InterPro: IPR001484; Pyrokinin.

DR PROSITE: PS00539; PYROKININ_1.

KW Neuropeptide; Amidation; Pyrokinin.

FT MOD_RES 8 AMIDATION.

SQ SEQUENCE 8 AA; 934 MW; 26341771A92AA87B CRC64;

Query Match 27.9%; Score 12; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.4e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PR 3 PR 4

Db 6 PR 7

RESULT 10

LPK_LBUMA STANDARD; PRT; 8 AA.

AC P13019; ID LPK_LBUMA

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DB Leucophphaea maderae (LPK) (LEM-PK).

OS Leucophphaea maderae (Madeira cockroach).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neopota; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;

OC Blaberidae; Leucophphaea.

NCBI_TaxID=6988;

RN [1]

RP SEQUENCE.

RA MEDLINE=852269041; PubMed=3015140;

RT "Active fragments and analogs of the insect neuropeptide leucopyrokinin: structure-function studies";

RT Biochem. Biophys. Res. Commun. 137:936-942 (1986).

RN [2]

RP TISSUE=Head;

RA MEDLINE=87052251; PubMed=2877794;

RT "Primary structure and synthesis of a blocked myotropic neuropeptide isolated from the cockroach, *Leucophaea maderae*.";

RT Comp. Biochem. Physiol. 85C:219-224 (1986).

RL CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic activity).

CC -!- MISCELLANEOUS: An analog without the N-terminal PCA residue was synthesized and found to exhibit greater activity (144%) than the parent neuropeptide. The portion of the sequence of LPK most critical for the myotropic properties is limited to the pentapeptide fragment FPLRL.

CC -!- SIMILARITY: Belongs to the pyrokinin family.

DR PIR: A22967; A23957.

DR InterPro: IPR001484; Pyrokinin.

DR PROSITE: PS00539; PYROKININ_1.

KW Neuropeptide; Amidation; Pyrokinin; Pyrrolidone carboxylic acid.

FT MOD_RES 1 PYRROLIDONE CARBOXYLIC ACID.

SQ SEQUENCE 8 AA; 949 MW; 92341771A05A1B6 CRC64;

Query Match 27.9%; Score 12; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.4e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PR 3 PR 4

Db 6 PR 7

RESULT 11

PPK3 PERAM STANDARD; PRT; 8 AA.

AC P82618; ID PPK3 PERAM

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DB Pyrokinin-3 (Pea-PK-3) (FXPRL-amide).

OS Periplaneta americana (American cockroach).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea; Blattidae; Periplaneta.

NCBI_TaxID=6978;

RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.

RC TISSUE=Retrocebral complex;

RN [1]

RA MEDLINE=99112460; PubMed=10136736;

RA Predel R.; Keiner R.; Nachman R.J.; Holman G.M.; Rapus J.; Gaede G.; RT "Differential distribution of pyrokinin-isoforms in cerebral and abdominal neuromechanical organs of the American cockroach.";

RT Insect Biochem. Mol. Biol. 29:139-144 (1999).

RN [2]

RP TISSUE SPECIFICITY.

RA Predel R.; Eckert M.; MEDLINE=20189834; PubMed=10723010;

RA RT "Tagma-specific distribution of FXPRLamides in the nervous system of the American cockroach.";

RT J. Comp. Neuro. 419:352-363 (2000).

RL CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic activity).

CC -!- TISSUE SPECIFICITY: Corpora cardiaca.

CC -!- MASS SPECTROMETRY: MW=996.5; METHOD=MALDI.

CC -!- SIMILARITY: Belongs to the Pyrokinin family.

KW Neuropeptide; Amidation; Pyrokinin.

FT MOD_RES 8 AMIDATION.

SQ SEQUENCE 8 AA; 997 MW; 0B34177409D772C7 CRC64;

Query Match 27.9%; Score 12; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.4e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PR 4

Db 6 PR 7

RESULT 12

RS7 MYCIT STANDARD; PRT; 8 AA.

AC P33544; ID RS7 MYCIT

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DB 30S ribosomal protein S7 (Fragment).

GN RPSG

OS Mycobacterium intracellulare.

OC Bacteria; Actinobacteria; Actinomycetales;

OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.

NCBI_TaxID=1767;

RN SEQUENCE FROM N.A.

RP MEDLINE=93197130; PubMed=8451173;

RA Nair J.; Rouse D.A.; Morris S.L.; RT "Nucleotide sequence analysis of the ribosomal S12 gene of Mycobacterium intracellulare.";

RT Nucleic Acids Res. 21:1039-1039 (1993).

CC -!- FUNCTION: One of the primary rRNA binding proteins, it binds directly to 16S rRNA where it nucleates assembly of the head domain of the 30S subunit. Is located at the subunit interface close to the decoding center, probably blocks exit of the E-site tRNA (By similarity).

CC -!- SUBUNIT: Part of the 30S ribosomal subunit. Contacts proteins S9

and S11 (By similarity): Belongs to the S7P family of ribosomal proteins.

-1- SIMILARITY: Belongs to the S7P family of ribosomal proteins.

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CC EMBL; L0171; AA25376.1; -.

CC DR; S35538; S35538.

CC PIR; S35538; S35538.

CC HANAP; MP_00480; -1.

CC InterPro; IPR00235; Ribosomal_S7.

CC PROSITE; PS00052; RIBOSOMAL_S7_PARTIAL.

CC DR; KW; Ribosomal protein; RNA-binding; tRNA-binding; tRNA-binding.

CC FT; INIT-MET 0 BY SIMILARITY.

CC FT; NON-TER 8 0 MW; 850 MW;

CC SQ; SEQUENCE 8 AA; 63276DC768732417 CRC64;

CC Query Match 27.9%; Score 12; DB 1; Length 8;

CC Best Local Similarity 100.0%; Pred. No. 1.4e+05; Mismatches 0;

CC Indels 0; Gaps 0;

CC Qy 3 PR 4

CC Db 1 PR 2

RESULT 13

CC UC26_MAIZE STANDARD; PRT; 8 AA.

CC AC; P8052;

CC DT; 01-OCT-1996 (Rel. 34, Created)

CC DT; 01-OCT-1996 (Rel. 34, Last sequence update)

CC DT; 15-MAR-2004 (Rel. 43, Last annotation update)

CC DB; Unknown protein from 2D-page of etiolated coleoptile (Spot 907)

CC DE; (Fragment).

CC OS; Zea mays (Maize)

CC Eukaryota; Viridiplantae; Streptophytida; Embryophyta; Tracheophyta;

CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

CC PACCAD; Clade; Panicoideae; Andropogoneae; Zea.

CC NCBI_TAXID=4577; [1]

CC TISSUE=Coleoptile.

CC RA; Touze, P.; Riccardi, F.; Morin, C.; Damerval, C.; Huet, J.-C.,

CC RA; Pernollet, J.-C.; Zilly, M.; de Vienne, D.;

CC RT; "The maize two dimensional gel protein database: towards an integrated genome analysis program." /

CC RT; Theor. Appl. Genet. 93:937-1005 (1996).

CC -1- MISCELLANEOUS: On the 2D-gel the determined PI of this unknown

CC protein is: 7.0, its MW is: 57.2 kDa.

CC DR; Maize-2DPAGE; P80632; COLEOPTILE.

CC FT; NON-TER 1 1

CC FT; NON-TER 8 8 MW; 990 MW;

CC SQ; SEQUENCE 8 AA; 9639D6DAB4176B1D CRC64;

CC Query Match 27.9%; Score 12; DB 1; Length 8;

CC Best Local Similarity 100.0%; Pred. No. 1.4e+05; Mismatches 0;

CC Indels 0; Gaps 0;

CC Qy 3 PR 4

CC Db 3 PR 4

RESULT 14

CC UP01_HUMAN STANDARD; PRT; 8 AA.

CC ID; UP01_HUMAN

CC P30087;

CC DT; 01-APR-1993 (Rel. 25, Created)

CC and S11 (By similarity): Belongs to the S7P family of ribosomal proteins.

CC -1- SIMILARITY: Belongs to the S7P family of ribosomal proteins.

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CC EMBL; L0171; AA25376.1; -.

CC DR; S35538; S35538.

CC PIR; S35538; S35538.

CC HANAP; MP_00480; -1.

CC InterPro; IPR00235; Ribosomal_S7.

CC PROSITE; PS00052; RIBOSOMAL_S7_PARTIAL.

CC DR; KW; Ribosomal protein; RNA-binding; tRNA-binding; tRNA-binding.

CC FT; INIT-MET 0 BY SIMILARITY.

CC FT; NON-TER 8 0 MW; 850 MW;

CC SQ; SEQUENCE 8 AA; 63276DC768732417 CRC64;

CC Query Match 27.9%; Score 12; DB 1; Length 8;

CC Best Local Similarity 100.0%; Pred. No. 1.4e+05; Mismatches 0;

CC Indels 0; Gaps 0;

CC Qy 3 PR 4

CC Db 7 PR 8

RESULT 15

CC PSK_DAICA STANDARD; PRT; 5 AA.

CC ID; PSK_DAICA

CC AC; P58261;

CC DT; 16-OCT-2001 (Rel. 40, Created)

CC DT; 16-OCT-2001 (Rel. 40, Last sequence update)

CC DT; 16-OCT-2001 (Rel. 40, Last annotation update)

CC DE; Phytosulfokine-alpha (PSK-alpha) (Contains: Phytosulfokine-beta (PSK-beta)).

CC DE; Daucus carota (Carrot).

CC OS; Eukaryota; Viridiplantae; Streptophytida; Embryophyta; Tracheophyta;

CC Spermatophyta; Magnoliophyta; Eudicotyledons; core eudicots; asterids;

CC OC; Daucus carota (Carrot).

CC OC; Spermatophyta; Magnoliophyta; Eudicotyledons; core eudicots; asterids;

CC OC; campnulids; Apiales; Apiaceae; Apioideae; Daucinae; Daucus.

CC OC; NCBI_TAXID=4039;

CC RN; SEQUENCE, AND IDENTIFICATION BY MASS SPECTROMETRY.

CC RC; SPRAINS-CV, US-Harumakiigosun;

CC RX; MEDLINE=2021743; PubMed=10750705;

CC RA; Kamada, H.; Sakagami, Y.; Matsuno, T.; Yamamoto, M.; Kobayashi, T.,

CC RT; "A secreted peptide growth factor, phytosulfokine, acting as a

CC stimulatory factor of carrot somatic embryo formation." /

CC RL; Plant Cell Physiol. 41:27-32 (2000).

CC CC; "FUNCTION: In presence of 2,4-D, stimulates proliferation of the

CC cells, but does not stimulate differentiation into the somatic

CC embryos. -1- SUBCELLULAR LOCATION: Secreted.

CC CC; Sulfation is important for activity and for the binding to a

CC putative membrane receptor (By similarity).

CC CC; -1- SIMILARITY: Belongs to the phytosulfokine family.

CC KW; Growth factor; Sulfation.

CC CC; -1- PEPTIDE; 1 4 SULFATION.

CC FT; MOD_RES 1 1 SULFATION.

CC FT; MOD_RES 3 3 SULFATION.

CC SQ; SEQUENCE 5 AA; 687 MW; 76C1BB504B300000 CRC64;

CC Query Match 25.6%; Score 11; DB 1; Length 5;

CC Best Local Similarity 100.0%; Pred. No. 1.4e+05; Mismatches 0;

CC Indels 0; Gaps 0;

Qy 7 IY 8
|
Db 2 IY 3

Search completed: July 28, 2004, 07:54:11
Job time : 14 secs

RESULT 4

P92393 PRELIMINARY; PRT; 7 AA.

ID P92393; AC P92393; DT 01-MAY-1997 (TREMBLrel. 03, Created) DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update) DB Ribosomal protein 11 (Fragment). GN RPS11. OS Chloroplast. OG Hordeum vulgare (Barley). OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Tracheae; Poaceae; Pooidae; Triticeae; Hordeum. OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Peridictyon sanctum. RN [1] -

SEQUENCE FROM N.A.

RC STRAIN=H3139; TISSUE=Leaf; MEDLINE=97271648; PubMed=9126564; RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA sequence data."; Petersen G., Seberg O.; RPL EMBL: Z77764; CAB01370.1; GO; GO:009507; C:chloroplast; IEA. XW Chloroplast.

FT NON TER 1 AA; 894 MW; 6734140333277700 CRC64;

SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 37.2%; Score 16; DB 8; Length 7; Best Local Similarity 66.7%; Pred. No. 1e+06; Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPR 4 |: Db 1 PPK 3

RESULT 5

P92430 PRELIMINARY; PRT; 7 AA.

ID P92430; AC P92430; DT 01-MAY-1997 (TREMBLrel. 03, Created) DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update) DB Ribosomal protein 11 (Fragment). GN RPS11. OS Lophopyrum elongatum (Tall wheatgrass). OG Chloroplast. OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Thinopyrum. RN [1] -

SEQUENCE FROM N.A.

RC STRAIN=H6592; TISSUE=Leaf; MEDLINE=97271648; PubMed=9126564; RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA sequence data."; Petersen G., Seberg O.; RPL EMBL: Z77743; CAB01307.1; GO; GO:009507; C:chloroplast; IEA. XW Chloroplast.

FT NON TER 1 AA; 894 MW; 6734140333277700 CRC64;

SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 37.2%; Score 16; DB 8; Length 7; Best Local Similarity 66.7%; Pred. No. 1e+06; Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPR 4 |: Db 1 PPK 3

SEQUENCE FROM N.A.

RC STRAIN=H6668; TISSUE=Leaf; MEDLINE=97271648; PubMed=9126564; RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA sequence data."; Petersen G., Seberg O.; RPL EMBL: Z77758; CAB01325.1; GO; GO:009507; C:chloroplast; IEA. XW Chloroplast.

FT NON TER 1 AA; 894 MW; 6734140333277700 CRC64;

SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 37.2%; Score 16; DB 8; Length 7; Best Local Similarity 66.7%; Pred. No. 1e+06; Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPR 4
Db 1 PPK 3

RESULT 6
ID P92221; PRELIMINARY; PRT; 7 AA.
AC P92221; 03, Created
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-MAY-1997 (TREMBLrel. 03, Last annotation update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Bromus inermis (Smooth brome grass).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC NCBI_TaxID=15371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OSA14; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data";
RT Mol. Phylogenet. Evol. 7:217-230(1997).
RL EMBL; Z77759; CAB01355.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;
Query Match 37.2%; Score 16; DB 8; Length 7;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 PPR 4
Db 1 PPK 3

RESULT 7
ID P92425; PRELIMINARY; PRT; 7 AA.
AC P92425; 03, Created
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-MAY-1997 (TREMBLrel. 03, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Pseudoroegneria spicata (Bluebunch wheatgrass) (Agropyron spicatum).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Pseudoroegneria.
OC NCBI_TaxID=4604;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H9002; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data";
RT Mol. Phylogenet. Evol. 7:217-230(1997).
RL EMBL; Z77744; CAB01310.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;
Query Match 37.2%; Score 16; DB 8; Length 7;

Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPR 4
Db 1 PPK 3

RESULT 8
ID P92381; PRELIMINARY; PRT; 7 AA.
AC P92381; 03, Created
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Hordeum brachyantherum.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC NCBI_TaxID=52712;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data";
RT Mol. Phylogenet. Evol. 7:217-230(1997).
RL EMBL; Z77761; CAB01367.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;
Query Match 37.2%; Score 16; DB 8; Length 7;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPR 4
Db 1 PPK 3

RESULT 9
ID P92387; PRELIMINARY; PRT; 7 AA.
AC P92387; 03, Created
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Hordearia persica.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC NCBI_TaxID=37678;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=15556; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data";
RT Mol. Phylogenet. Evol. 7:217-230(1997).
RL EMBL; Z77748; CAB01322.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;
Query Match 37.2%; Score 16; DB 8; Length 7;

DR GO:0009507; C:chloroplast; IEA.

KW Chloroplast.

FT NON TER 1

SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 37.2%; Score 16; DB 8; Length 7;

Best Local Similarity 66.7%; Pred. No. 1e+06;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPR 4
|:
Db 1 PPK 3

RESULT 10

P92210 PRELIMINARY; PRT; 7 AA.

AC P92210; PRT; 7 AA.

DT 01-MAY-1997 (TREMBLrel. 03, Created)

DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE Ribosomal protein 11 (Fragment).

OS Agropyron cristatum (Crested wheatgrass).

CHLOROPLAST.

OC BUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES; POACEAE; POOIDEAE; AUSTRALOXYTRIUM RETROFRACTUM.

OS CHLOROPLAST.

OC BUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES; POACEAE; POOIDEAE; OC TRITICEAE; AUSTRALOXYTRIUM.

NCBI_TAXID=4597;

RN [1]

RP SEQUENCE FROM N.A.

NCBI_TAXID=4597;

RX MEDLINE=97271648; PUBMED=9126564;

RX STRAIN=H4349; TISSUE=Leaf;

RX PDB=1H4349; TISSUE=Leaf;

Petersen G., Seberg O.; "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA sequence data.," Mol. Phylogenet. Evol. 7:217-230(1997).

EMBL; Z77771; CAB03391.1; -.

GO; GO:0009507; C:chloroplast; IEA.

CHLOROPLAST.

FT NON TER 1

SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 37.2%; Score 16; DB 8; Length 7;

Best Local Similarity 66.7%; Pred. No. 1e+06;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPR 4
|:
Db 1 PPK 3

RESULT 11

P92440 PRELIMINARY; PRT; 7 AA.

AC P92440; PRT; 7 AA.

DT 01-MAY-1997 (TREMBLrel. 03, Created)

DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE Ribosomal protein 11 (Fragment).

OS THINOPYRUM BESSARABICUM.

CHLOROPLAST.

OC BUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES; POACEAE; POOIDEAE; OC TRITICEAE; THINOPYRUM.

NCBI_TAXID=4601;

RN [1]

RP SEQUENCE FROM N.A.

STRAIN=H6725; TISSUE=Leaf;

PDB=1H6725; TISSUE=Leaf;

MEDLINE=97271648; PUBMED=9126564;

Petersen G., Seberg O.; "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA sequence data.," Mol. Phylogenet. Evol. 7:217-230(1997).

EMBL; Z77769; CAB03385.1; -.

CHLOROPLAST.

OC BUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES; POACEAE; POOIDEAE; OC TRITICEAE; HETERANTHELIUM.

NCBI_TAXID=37659;

RN [1]

RP SEQUENCE FROM N.A.

STRAIN=H5557; TISSUE=Leaf;

MEDLINE=97271648; PUBMED=9126564;

Petersen G., Seberg O.; "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA sequence data.," Mol. Phylogenet. Evol. 7:217-230(1997).

EMBL; Z77769; CAB03385.1; -.

RT sequence data.";

RL Mol. Phylogenet. Evol. 7:217-230(1997).

DR EMBL; 27750; CAB0328.1; -.

DR GO; GO:0009507; C:chloroplast; IEA.

KW Chloroplast.

FT NON-TER 1 1

SEQUENCE 7 AA; 894 MW; 673414033327700 CRC64;

Query Match 37.2%; Score 16; DB 8; Length 7;

Best Local Similarity 66.7%; Pred. No. 1e+06;

Matches 2; Conservative 1; Mismatches 0; Indels 0;

Gaps 0;

Qy 2 PPR 4

Db 1 PPK 3

RESULT 14

RP P92372 PRELIMINARY; PRT; 7 AA.

AC P92372;

DT 01-MAY-1997 (TREMBLrel. 03, Created)

DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE Ribosomal protein 11 (Fragment).

GN RPS11.

OS Haynaldia villosa.

OG Chloroplast.

CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

CC PACCAD clade; Panicoidae; Andropogoneae; Haynaldia.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=H5561; TISSUE=Leaf;

RC MEDLINE=97271648; PMID=9126564;

RA Petersen G.; Seberg O.;

RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA sequence data.";

RT Mol. Phylogenet. Evol. 7:217-230(1997).

RL EMBL; 277741; CAB01301.1; -.

DR GO; GO:0009507; C:chloroplast; IEA.

KW Chloroplast.

FT NON-TER 1 1

SEQUENCE 7 AA; 894 MW; 673414033327700 CRC64;

Query Match 37.2%; Score 16; DB 8; Length 7;

Best Local Similarity 66.7%; Pred. No. 1e+06;

Matches 2; Conservative 1; Mismatches 0; Indels 0;

Gaps 0;

Qy 2 PPR 4

Db 1 PPK 3

RESULT 15

RP P92442 PRELIMINARY; PRT; 7 AA.

AC P92442;

DT 01-MAY-1997 (TREMBLrel. 03, Created)

DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE Ribosomal protein 11 (Fragment).

GN RPS11.

OS Taeniatherum caput-medusae (Medusaead).

CG Chloroplast.

CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;

CC Triticeae; Taeniatherum.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=H10254; TISSUE=Leaf;



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OM protein - protein search, using SW model

Run on: July 28, 2004, 07:15:39 ; Search time 50 seconds

(without alignments)

45.208 Million Cell updates/sec

Perfect score: 43

Sequence: 1 qppraaiy 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters:

122046

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	43	100.0	8	3	AAB19055	Aab19055 Amino aci
2	38	88.4	8	2	AAV28537	AAV28537 Beta-1 in
3	36	83.7	8	2	AAW06877	AAW06877 Glycosami
4	33	76.7	7	2	AAV28538	AAV28538 Beta-1 in
5	31	72.1	8	2	AAR59581	AAR59581 Fibronect
6	31	72.1	8	2	AAR56244	AAR56244 Fibronect
7	31	72.1	8	2	AAT78582	AAT78582 Fibronect
8	31	72.1	8	2	AAV83682	AAV83682 33 kd fib
9	31	72.1	8	2	AAW46437	AAW46437 Synthetic
10	31	72.1	8	2	AAW19843	AAW19843 Chimeric
11	31	72.1	8	2	AAW73537	AAW73537 Fibronect
12	31	72.1	8	2	AAW81843	AAW81843 Fibronect
13	31	72.1	8	2	AAV32881	AAV32881 Fibronect
14	31	72.1	8	2	AAV32869	AAV32869 Fibronect
15	31	72.1	8	2	AAV28545	AAV28545 Beta-1 in
16	31	72.1	8	4	AAB91965	AAB91965 Fibronect
17	31	72.1	8	4	AAB91982	AAB91982 Fibronect
18	28	65.1	6	2	APR62181	APR62181 UI_SIRNP
19	28	65.1	6	2	AAR73883	AAR73883 Rubella v
20	26	60.5	6	2	AAY28511	AAY28511 Beta-1 in
21	26	60.5	6	3	AAB19055	AAB19055 Amino aci
22	25	58.1	7	2	AAR73902	AAR73902 Streptococ
23	25	58.1	7	7	ADC44364	ADC44364 Endotheli
24	25	58.1	8	2	AAY40669	AAY40669 A2 deriva
25	58.1	8	3	AAV30008	AAV30008 Scaffold	

ALIGNMENTS

2.6	24	55.8	7	2	AAR73879	Rubella v
2.7	23	53.5	7	2	AAG98209	Human SNP
2.8	23	53.5	7	2	AAR09404	IFPA-1 alp
2.9	23	53.5	7	7	ADC28167	Synthetic
3.0	22	51.2	7	7	AAR34386	PRB subst
3.1	22	51.2	7	3	AAW71730	Peptide #
3.2	22	51.2	7	3	AAY95265	Crosssite
3.3	22	51.2	7	4	AAB99790	Protein k
3.4	22	51.2	7	4	AAG65169	AKT inhib
3.5	22	51.2	7	4	AAB82202	PKA inhib
3.6	22	51.2	7	4	AAB59271	Phosphory
3.7	22	51.2	7	5	AAG66179	Peptide s
3.8	22	51.2	7	6	AAO19502	KMT inhib
3.9	22	51.2	7	7	ABU08523	Protein k
4.0	22	51.2	7	7	ADC81657	Pyrazole
4.1	22	51.2	7	7	ADE49662	
4.2	22	51.2	8	2	AAR32362	Sample pe
4.3	22	51.2	8	2	ABB76926	Cyclocontext
4.4	22	51.2	8	2	AAY33180	Human PSF
4.5	22	51.2	8	2	AAY48023	Immunogen

They are also useful for the treatment of stroke, a burn type injury, cancer, and osteoporosis.

1 OPPRARIY 8

KW Beta 1 integrin dependent cell adhesion; LipPar motif; tumour;
 KW C-terminal tyrosine tagged; cancer; fibronectin; melanoma.
 XX
 OS Synthetic.
 XX
 PA WO937669-A1.
 XX
 PD 29-JUL-1999.
 XX
 PF 21-JAN-1999; 99WO-US001236.
 XX
 PR 22-JAN-1998; 98US-0072119P.
 PR 12-AUG-1998; 98US-0092211P.
 PR 12-AUG-1998; 98US-0096212P.
 PA (MINU) UNIV MINNESOTA.
 XX
 PI McCarthy JB, Furcht LT, Brienzzo A;
 XX
 DR WPI; 1999-469112/39.
 XX
 PT New peptides modulating beta1 integrin subunit dependent cell adhesion,
 PT useful to study cell adhesion e.g. alpha4beta1 integrin dependent
 adhesion important in tumor cell biology.
 XX
 PS Example 4; Fig 7; 47PP; English.
 XX
 CC This sequence is a C-terminal tyrosine tagged peptide. This peptide
 CC inhibits beta-1 integrin subunit dependent cell adhesion. Peptides
 CC AAY28510-Y28549 have been used to show that peptides which modulate this
 CC form of cell adhesion need a C-terminal amino acid residue (Ar) which has
 CC a side chain including an aromatic group, and a Penultimate C-terminal
 CC amino acid residue (Lip) with an alkyl side chain group, i.e. a 'LipAr'
 CC motif. Studies with these peptides have also shown that inhibiting
 CC peptides do not contain D-amino acids and that it is the presence of the
 CC ArLip motif that conveys effective beta1 integrin dependent cell adhesion
 CC inhibition. The beta-1 integrin subunit dependent cell adhesion is
 CC important for cell adhesion to extracellular matrix proteins, and the
 CC subunit is expressed on tumours such as melanomas. Therefore these LipAr
 CC motif containing peptides may be important in the treatment of cancer
 XX
 SQ Sequence 7 AA;
 Query Match 76.7%; Score 33; DB 2; Length 7;
 Best Local Similarity 85.7%; Pred. No. 1.4e-06;
 Matches 6; Conservative 0; N mismatches 1; Indels 0; Gaps 0;
 OS Synthetic.
 XX
 OY 2 PPRAAAY 8
 DB 1 PPRARY 7
 XX
 AC AAR59381;
 DT 25-MAR-2003 (revised)
 DT 22-MAR-1993 (first entry)
 XX
 DE Fibronectin fragment FN5.
 XX
 KW Fibronectin; retro virus; HIV; AIDS; virucide; ovalbumin.
 XX
 OS Synthetic.
 XX
 PA WO9417097-A1.
 XX
 PD 04-AUG-1994.
 XX
 PR 19-JAN-1994; 94WO-US000729.
 XX
 PR 19-JAN-1993; 93US-00006121.
 XX
 PA (MINU) UNIV MINNESOTA.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Wahl SM, McCarthy JB, Furcht LT;
 XX
 DR WPI; 1994-264029/32.
 XX
 PT New polypeptide comprising carrier molecule coupled to fibronectin
 PT fragment - useful in treatment of retroviral infections and associated
 diseases, e.g. AIDS.
 XX
 PS Claim 1; Page 13; 18PP; English.
 XX
 CC This peptide may be covalently linked to a carrier (especially
 CC ovalbumin). The resulting compound FN-CH-V has excellent HIV virus
 CC inhibiting activity, low toxicity and high safety. It may be useful in
 CC the treatment of AIDS. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 8 AA;
 Query Match 72.1%; Score 31; DB 2; Length 8;
 Best Local Similarity 85.7%; Pred. No. 1.4e-06;
 Matches 6; Conservative 0; N mismatches 1; Indels 0; Gaps 0;
 OS Synthetic.
 OY 1 OPPRAAI 7
 DB 2 QPFRARI 8
 XX
 AC AAR56244 standard; peptide; 8 AA.
 XX
 AC AAR56244;
 XX
 DT 25-MAR-2003 (revised)
 DT 12-JAN-1995 (first entry)
 XX
 DE Fibronectin-derived peptide.
 XX
 KW Fibronectin; inflammation; antiinflammatory; immunosuppressive;
 KW leukocyte; arthritis; autoimmune disease; graft versus host disease.
 XX
 PA (MINU) UNIV MINNESOTA.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Furcht LT, McCarthy JB, Wahl SM, Allen JB;
 XX
 DR WPI; 1994-217799/26.
 XX
 PT Fibronectin derived peptide(s) for treating inflammation - involving
 PT leucocyte activation, Partic. arthritis and graft versus host disease.
 XX
 PS Claim 8; Page 31; 45PP; English.
 XX
 CC Chronic inflammation or autoimmune diseases are treated with peptides
 CC corresponding to residues 1906-24 (AAR56242), 1946-60 (AAR56243), 1892-99
 CC (AAR56244), 1961-85 (AAR56245), 1781-92 (AAR56246) and 1485-504
 CC (AAR56247) of fibronectin. (Updated on 25-MAR-2003 to correct PN field.)
 XX

PR 01-MAY-1996; 96US-00642250.
 XX
 PA (UYRQ) UNIV ROCKEFELLER.
 XX
 Masure HR, Rosenow CI, Tuomanen E, Wizeman TM;
 PI
 XX
 WPI; 1997-549682/50.
 XX
 New isolated streptococcal choline binding proteins - used to develop
 PT products for treating bacterial infection and for
 PT detection, diagnosis and screening.
 XX
 Claim 34; Page 14; 142pp; English.
 XX
 The present sequence represents a synthetic peptide, Fns. Streptococcus
 CC pneumoniae (pneumococci) adheres to fibronectin at a site within the
 CC carboxy-terminal heparin II binding domain. An eight amino acid stretch
 CC within the type III #14 repeat supports adherence. The present peptide is
 CC based on these amino acids. S. pneumoniae binds directly to this peptide.
 CC An antibody to Fns inhibits adherence of S. pneumoniae to whole
 CC fibronectin by greater than 70%. The peptide can be used to prepare
 CC vaccines. The antibodies can be used for passive immunisation,
 CC diagnostics, or screening. The peptide can also be used for treating or
 CC preventing bacterial infection
 XX
 Sequence 8 AA;

Query Match 72.1%; Score 31; DB 2; Length 8;
 Best Local Similarity 85.7%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7
 Db 2 QPPRAI 8

RESULT 11
 AAW73537

ID AAW73537 standard; peptide; 8 AA.

XX
 AC AAW73537;

XX
 DT 04-MAR-1999 (first entry)

XX
 DE Fibronectin fragment, Peptide FN-C/H-V.

XX
 KW Adhesion promoter; extra-cellular matrix peptide;

XX
 KW bimolecule immobilisation; fibronectin.

XX
 OS Synthetic.

XX
 PN US8853744-A.

XX
 PD 29-DEC-1998.

XX
 PF 20-AUG-1996; 96US-00699965.

XX
 PA (MINN) UNIV MINNESOTA.

XX
 PI Mocradian DL, Fields GB;

XX
 DR WPP; 1999-094819/08.

XX
 PT Solid-phase method for modifying substrate with peptide, especially

CC adhesion-promoting peptide - applied to medical devices, e.g. vascular

CC grafts, uses peptide modified by photoreactive group for covalent

CC attachment.

XX
 PS Claim 4; Fig 1; 14pp; English.

XX
 CC This sequence represents a fragment of fibronectin, and is designated

CC peptide FN-C/H-V. This sequence is an adhesion promoting extra-cellular

CC matrix peptide, and can be used in the method of the invention. The

CC method is a solid-phase method for modifying a substrate surface to

CC include a biomolecule (1), and comprises: (a) providing an immobilised

CC (1), comprising a peptide having: (i) an N alpha-terminus; or (ii) an

CC active site, by covalently attaching it to a support; (b) attaching a

CC photoreactive crosslinking agent (1), having at least one photoreactive

CC group, to the immobilised peptide, in (i) at the N alpha-terminus or in

CC (ii) to the peptide at an amino acid that does not form part of the

CC active site; (c) removing the photoreactive analogue (1a) of (1) from the

CC support; and (d) attaching (1a) to a solid surface by activating the

PR 05-JUN-1997.
 XX
 PA 96WO-US019150.
 XX
 WPI; 27-NOV-1996;
 XX
 96US-00561368.
 PR 28-NOV-1995;
 PR 21-AUG-1996;
 PR 21-AUG-1996;
 PR 21-AUG-1996;
 XX
 PA (GENV) GENVEC INC.

XX
 Wickham TJ, Kovacs I, Brough DE;
 PI
 XX
 DR WPI; 1997-310665/28.
 XX
 PT Adenoviral vectors containing chimeric coat protein - bind and enter
 PT cells more efficiently, useful for gene therapy of e.g. cancer,
 PT auto-immune diseases, etc.
 XX
 PA (GENV) Page 19; 121pp; English.

photoreactive group. The method is particularly used to immobilise (I) on medical devices, specifically adhesion-promoting peptides on vascular grafts such that adhesion of cells to the device is improved. More generally a wide range of peptides can be deposited on blood oxygenators, pumps or sensors; tubing; stents; pacemaker leads; heart valves; catheters; artificial organs; or body implants generally. Bound (I) retains its native activity, specifically promotion of adhesion and spreading of vascular endothelial cells. The method ensures that (II) reacts with alpha-amino groups only (contrast use of soluble peptide where reaction may occur at epsilon-amino groups in the active site) and a large excess of (II) can be used to avoid wasting peptide

SQ Sequence 8 AA;

Query Match 72.1%; Score 31; DB 2; Length 8;
 Best Local Similarity 85.7%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7

2 QPPRAKI 8

RESULT 12
 AAW81843 standard; peptide; 8 AA.
 XX
 AC AAW81843;
 XX
 DT 17-OCT-2003 (revised)
 05-FBB-1999 (first entry)

DE Fibronectin-like peptide V.
 XX
 KW Fibronectin; ischemia; treatment; inflammatory disease; A chain;
 XX
 heparin-binding; RGDs-mediated cell adhesion region.
 OS unidentified.

XX
 PN US5840691-A.
 XX
 PD 24-NOV-1998.

XX
 PR 07-JUN-1995; 95US-00480133.
 PR 10-DEC-1992; 92US-00990296.
 PR 21-OCT-1993; 93US-00139903.

XX
 PA (FURC/) FURCHT L. T.
 PA (WAHL/) WAHL S. M.
 PA (ALLE/) ALLEN J. B.
 PA (BILL/) BILLUPS K. L.
 PA (MCCA/) MCCARTHY J. B.
 PA (EVER/) EVERETT J. E.

XX
 Allen JB, Wahl SM, Everett JE, McCarthy JB, Furcht LT;
 PI Billups KL;
 XX
 DR WPI; 1999-034077/03.

XX
 Treatment of ischaemia - with fibronectin peptides.

XX
 Claim 1; Col 25-26; 352P; English.
 XX
 AAW81841-W81846 are peptides used in a method for treating ischemia using

CC polypeptides with fibronectin activity. The method can be used for
 CC treating a number of disease such as those associated with inflammatory
 CC disease by administering an effective amount of a composition containing
 CC a polypeptide having a sequence of at least 3 amino acids corresponding
 CC substantially to an amino acid sequence within the 33 kD carboxyl
 CC terminus containing amino acid sequence located on the A chain of fibronectin or
 CC an RGD-containing amino acid sequence within the 11.5 kD RGDS-mediated
 CC cell adhesion region located on all isoforms of fibronectin. (Updated on

CC 17-OCT-2003 to standardise OS field)

CC XX Sequence 8 AA;
 CC Query Match 72.1%; Score 31; DB 2; Length 8;
 CC Best Local Similarity 85.7%; Pred. No. 1.4e+06;
 CC Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 CC SQ Sequence 8 AA;

CC Query Match 72.1%; Score 31; DB 2; Length 8;
 CC Best Local Similarity 85.7%; Pred. No. 1.4e+06;
 CC Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 CC SQ Sequence 8 AA;

CC Fibronectin protein heparin II binding domain peptide H-V.

CC DE Fibronectin; extracellular matrix; open wound healing; IIICS domain;
 CC KW acute Gaping cutaneous wound; chronic cutaneous ulcer; therapy;
 CC wound healing; Promoter; cell binding domain; heparin II binding domain.

CC XX DT 02-NOV-1999 (first entry)
 CC DE XX
 CC DE Fibronectin protein heparin II binding domain peptide H-V.

CC OS Homo sapiens.
 CC PN WO9942117-A1.
 CC XX PD 26-AUG-1999.

CC XX PF 10-FEB-1999;
 CC XX PR 18-FEB-1998;
 CC XX PA (UYN) UNTV NEW YORK STATE RES FOUND.

CC XX Clark RA, Greiling D;
 CC XX DR WPI; 1999-527445/44.

CC XX PT New extracellular matrix used to accelerate healing of acute gaping
 CC cutaneous wounds and chronic cutaneous ulcers.

CC XX PS Claim 14; Page 19; 43pp; English.

CC This sequence represents a fibronectin protein fragment used in the
 CC extracellular matrix of the invention. The extracellular matrix comprises
 CC two or more fibronectin domains in the backbone matrix, and is used to
 CC enhance wound healing. The fibronectin domain peptides used are
 CC preferably from the IIICS domain, the cell binding domain, or the heparin
 CC II binding domain of human fibronectin. The matrix facilitates wound
 CC healing by providing an environment that intrinsically recruits new
 CC tissue cells to the wound site. The new matrix is useful for facilitating
 CC wound healing, especially useful for treating open wounds such as acute
 CC gaping cutaneous wounds and chronic cutaneous ulcers. The problem of
 CC chronic, non-healing wounds is severe. These open wounds require long-
 CC term care and procedures that are costly and labour intensive.
 CC Furthermore, these wounds have a severe impact on the patients' quality of
 CC life. Prior compositions and matrices have not been useful or cost
 CC effective. The present invention provides a matrix for wound healing that
 CC meets these requirements, and overcomes the deficiencies of the prior
 CC matrices

CC XX SQ Sequence 8 AA;

CC Query Match 72.1%; Score 31; DB 2; Length 8;

CC Best Local Similarity 85.7%; Pred. No. 1.4e+06;

CC Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CC SQ Sequence 8 AA;

CC Query 1 QPPRAAI 7



GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 28, 2004, 07:55:00 ; Search time: 41 Seconds

(without alignments)
 61.206 Million cell updates/sec

Title: SEQ3

Perfect score: 43

Sequence: 1 qppraaiy 8

Scoring table: BLOSUM62

GapPen 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313582936 residues

Total number of hits satisfying chosen parameters: 67706

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA: *

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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep;*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep;*
10: /cor2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep;*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	31	72.1	8	9 US-09-765-614B-6	Sequence 6, Appli
2	31	72.1	8	9 US-09-925-715-2	Sequence 2, Appli
3	31	72.1	8	10 US-09-999-724-58	Sequence 5, Appli
4	31	72.1	8	10 US-09-829-382-51	Sequence 11, Appli
5	31	72.1	8	14 US-10-017-193-4	Sequence 4, Appli
6	31	72.1	8	16 US-10-722-075-6	Sequence 6, Appli
7	28	65.1	8	9 US-09-165-614B-3	Sequence 3, Appli
8	28	65.1	8	16 US-10-722-075-3	Sequence 3, Appli
9	25	58.1	7	14 US-10-726-457-92	Sequence 92, Appli
10	24	55.8	7	16 US-10-346-737A-6	Sequence 6, Appli
11	23	53.5	7	10 US-09-954-385-360	Sequence 30, Appli
12	23	53.5	7	14 US-10-021-660-20	Sequence 90, Appli
13	22	51.2	7	9 US-09-845-667-6	Sequence 6, Appli
14	22	51.2	7	9 US-09-845-667-21	Sequence 21, Appli
15	22	51.2	7	9 US-09-845-667-56	Sequence 56, Appli

ALIGNMENTS

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RESULT 1
US-09-765-614B-6
; Sequence 6, Application US/09765614B
; Patent No. US201002215A1
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to
; TITLE OF INVENTION: diagnostic/therapeutic
; TITLE OF INVENTION: agents
; FILE REFERENCE: REF/Klavenvness/054
; CURRENT APPLICATION/US10-09-765-614B
; CURRENT FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence: Fibronectin
US-09-765-614B-6
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Query Match 72.1% ; Score 31; DB 9; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Gaps 0;
Qy 1 QPPRAAI 7
Db 2 QPSRARI 8
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RESULT 2
US-09-925-715-2
; Sequence 2, Application US/09925715
; Patent No. US201002217A1
; GENERAL INFORMATION:
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APPLICANT: Nycomed Imaging AS
 TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
 TITLE OF INVENTION: agents
 PILL REFERENCE: REF/Klavness/206
 CURRENT APPLICATION NUMBER: US/09/925,715
 CURRENT FILING DATE: 2001-08-10
 NUMBER OF SEQ ID NOS: 27
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 2
 LENGTH: 8
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE: Description of Artificial Sequence: Fibronectin
 OTHER INFORMATION: Peptide

US-09-925-715-2

Query Match Score 31; DB 9; Length 8;
 Best Local Similarity 85.7%; Pred. No. 1.2e+06;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QPPRAI 7
 Db 2 QPPRAI 8

RESULT 3
 US-09-999-724-58
 Sequence 58, Application US/09999724
 Publication No. US20030022355A1
 GENERAL INFORMATION:
 APPLICANT: WICKHAM, THOMAS J.
 APPLICANT: KOVSEDI, IMRE
 APPLICANT: BROUD, DOUGLAS E.
 TITLE OF INVENTION: VECTORS AND METHODS FOR GENE TRANSFER
 FILE REFERENCE: 2129860
 CURRENT APPLICATION NUMBER: US/09/999,724
 CURRENT FILING DATE: 2001-10-24
 PRIOR APPLICATION NUMBER: US 09/101,751
 PRIOR FILING DATE: 1999-01-29
 PRIOR APPLICATION NUMBER: WO 96US19150
 PRIOR FILING DATE: 1996-11-27
 PRIOR APPLICATION NUMBER: US 08/700,846
 PRIOR FILING DATE: 1996-08-21
 PRIOR APPLICATION NUMBER: US 08/701,124
 PRIOR FILING DATE: 1996-08-21
 PRIOR APPLICATION NUMBER: US 08/563,368
 PRIOR FILING DATE: 1995-11-28
 NUMBER OF SEQ ID NOS: 94
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 58
 LENGTH: 8
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE: Synthetic

OTHER INFORMATION: Synthetic
 US-09-999-724-58

Query Match Score 31; DB 10; Length 8;
 Best Local Similarity 85.7%; Pred. No. 1.2e+06;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QPPRAI 7
 Db 2 QPPRAI 8

RESULT 4
 US-09-829-382-11
 Sequence 11, Application US/09929382
 Publication No. US20030175293A1
 GENERAL INFORMATION:
 APPLICANT: Masure, H. Robert

APPLICANT: Rosendorff, Carsten I.
 TITLE OF INVENTION: Cholin, Theresa M.
 PILL REFERENCE: ANTI-PNEUMOCOCCAL VACCINES
 CURRENT APPLICATION NUMBER: 25
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: David A. Jackson, Esq.
 STREET: 411 Hackensack Ave, Continental Plaza, 4th
 Floor
 CITY: Hackensack
 STATE: New Jersey
 COUNTY: USA
 ZIP: 07601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/829,382
 FILING DATE: 09-Apr-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/847,065
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26-742
 REFERENCE/DOCKET NUMBER: 600-1-158 .
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-343-5100
 TELEFAX: 201-343-1684
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: Linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 SEQUENCE DESCRIPTION: SEQ ID NO: 11:
 US-09-829-382-11
 Query Match Score 31; DB 10; Length 8;
 Best Local Similarity 85.7%; Pred. No. 1.2e+06;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QPPRAI 7
 Db 2 QPPRAI 8

RESULT 5
 US-10-017-193-4
 Sequence 4, Application US/10017193
 Publication No. US2003113478A1
 GENERAL INFORMATION:
 APPLICANT: Dang, Mai Huong
 APPLICANT: Chiu, Phillip
 TITLE OF INVENTION: Surface Coating Method and Coated Device
 FILE REFERENCE: 52200-8010
 CURRENT APPLICATION NUMBER: US/10/017,193
 CURRENT FILING DATE: 2001-12-12
 NUMBER OF SEQ ID NOS: 10
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 4
 LENGTH: 8
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: attachment peptide from fibronectin

US-10-017-193-4
 Query Match 72.1%; Score 31; DB 14; Length 8;
 Best Local Similarity 85.7%; Pred. No. 1.2e+06;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 SEQ ID NO: 3
 LENGTH: 8
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial
 OTHER INFORMATION: Sequence: Fibronectin
 OTHER INFORMATION: peptide
 US-10-722-075-6
 Query Match 72.1%; Score 31; DB 16; Length 8;
 Best Local Similarity 85.7%; Pred. No. 1.2e+06;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 SEQ ID NO: 6
 LENGTH: 8
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial
 OTHER INFORMATION: Sequence: Heparin-binding
 OTHER INFORMATION: peptide
 US-10-722-075-3
 Query Match 65.1%; Score 28; DB 16; Length 8;
 Best Local Similarity 71.4%; Pred. No. 1.2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 SEQ ID NO: 3
 LENGTH: 8
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial
 OTHER INFORMATION: Sequence: Heparin-binding
 OTHER INFORMATION: peptide
 US-10-722-075-92
 Query Match 65.1%; Score 28; DB 16; Length 8;
 Best Local Similarity 71.4%; Pred. No. 1.2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 SEQ ID NO: 3
 LENGTH: 8
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial
 OTHER INFORMATION: Sequence: Heparin-binding
 OTHER INFORMATION: peptide
 US-10-722-075-9
 Query Match 65.1%; Score 28; DB 16; Length 8;
 Best Local Similarity 71.4%; Pred. No. 1.2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 SEQ ID NO: 3
 LENGTH: 8
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial
 OTHER INFORMATION: Sequence: Heparin-binding
 OTHER INFORMATION: peptide
 US-09-765-614B-3
 Query Match 65.1%; Score 28; DB 9; Length 8;
 Best Local Similarity 71.4%; Pred. No. 1.2e+06;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 10
 US-10-346-737A-6
 Sequence 6, Application US/10346737A
 Publication No. US20040142379A1
 GENERAL INFORMATION:
 APPLICANT: St. Hilaire, Phaedria
 TITLE OF INVENTION: AFFINITY FISHING FOR LIGANDS AND PROTEIN RECEPTORS
 FILE REFERENCE: 11225.16US01
 CURRENT APPLICATION NUMBER: US/10/346,737A
 CURRENT FILING DATE: 2003-01-16
 NUMBER OF SEQ ID NOS: 50
 SOFTWARE: Patentin, version 3.1
 SEQ ID NO: 6
 LENGTH: 7
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Peptide Spacer
 US-10-346-737A-6

Query Match: 55.8%; Score: 24; DB: 16; Length: 7;
 Best Local Similarity: 80.0%; Pred. No.: 1.2e+06;
 Matches: 4; Conservative: 1; Mismatches: 0; Indels: 0; Gaps: 0;

Qy 1 QPPRA 5
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 Db 3 RPPRA 7

RESULT 11
 US-09-954-385-360
 Sequence 360, Application US/09954385
 Publication No. US2003010467A1
 GENERAL INFORMATION:
 APPLICANT: Aehle, Wolfgang
 APPLICANT: Baldwin, Toby L.
 APPLICANT: Van Gassel, Franciscus J.C.
 APPLICANT: Janssen, Giselle G.
 APPLICANT: Murray, Christopher J.
 APPLICANT: Wang, Huaming
 APPLICANT: Winetzyk, Deborah S.
 TITLE OF INVENTION: Binding Complexes
 FILE REFERENCE: GC600
 CURRENT APPLICATION NUMBER: US/09/954,385
 CURRENT FILING DATE: 2001-09-12
 NUMBER OF SEQ ID NOS: 433
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 360
 LENGTH: 7
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: binding peptide
 US-09-954-385-360

Query Match: 53.5%; Score: 23; DB: 10; Length: 7;
 Best Local Similarity: 100.0%; Pred. No.: 1.2e+06;
 Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

Qy 2 PPR A 5
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 Db 4 PPR A 7

RESULT 12
 US-10-021-660-90
 Sequence 90, Application US/10021660
 Publication No. US20030152926A1
 GENERAL INFORMATION:
 APPLICANT: Murry, Richard
 APPLICANT: Glynn, Richard
 APPLICANT: Watson, Susan R.

APPLICANT: BOS Biotechnology, Inc.
 TITLE OF INVENTION: No. US20030152926A1 Methods of Diagnosis of Angiogenesis, Compositions and Methods of Screening For Angiogenesis
 TITLE OF INVENTION:
 FILE REFERENCE: 018501-00010US
 CURRENT APPLICATION NUMBER: US/10/021,660
 CURRENT FILING DATE: 2001-12-06
 PRIOR APPLICATION NUMBER: US/09/784,356
 PRIOR FILING DATE: 2001-02-14
 PRIOR APPLICATION NUMBER: US 09/637,977
 PRIOR FILING DATE: 2000-08-11
 NUMBER OF SEQ ID NOS: 135
 SEQ ID NO: 90
 LENGTH: 7
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: nuclear target motif
 US-10-021-660-90

Query Match: 53.5%; Score: 23; DB: 14; Length: 7;
 Best Local Similarity: 100.0%; Pred. No.: 1.2e+06;
 Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

Qy 2 PPR A 5
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 Db 1 PPR A 4

RESULT 13
 US-09-845-667-6
 Sequence 6, Application US/09845667
 Patent No. US2003006521A1
 GENERAL INFORMATION:
 APPLICANT: Cohen, Philip
 APPLICANT: Alessi, Dario
 APPLICANT: Cross, Darren
 TITLE OF INVENTION: CONTROL OF PROTEIN SYNTHESIS, AND SCREENING METHOD
 NUMBER OF SEQUENCES: 58
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Braman & Rogalsky, LLP
 STREET: P.O. Box 352
 CITY: Canandaigua
 STATE: New York
 COUNTRY: USA
 ZIP: 14424-0352
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/845,667
 FILING DATE: 30-Apr-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/091,763
 FILING DATE: 19-JUN-1998
 APPLICATION NUMBER: PCT/GB96/03186
 FILING DATE: 20-DEC-1996
 APPLICATION NUMBER: GB 9525083.2
 FILING DATE: 20-DEC-1995
 APPLICATION NUMBER: GB 9610272.8
 FILING DATE: 16-MAY-1996
 APPLICATION NUMBER: GB 9615066.9
 FILING DATE: 18-JUL-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Braman, Susan J.
 REGISTRATION NUMBER: 34,103
 REFERENCE/DOCKET NUMBER: 002.00041
 TELECOMMUNICATION INFORMATION:

TELEPHONE: 716-393-3002
 TELEFAX: 716-393-3001
 INFORMATION FOR SEQ ID NO: 6;
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Linear
 MOLECULE TYPE: Peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 6;
 US-09-845-667-6

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 Best Local Similarity 66.7%; Pred. No. 1.2e+06;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 PRAAY 8
 Db 2 PRAATF 7

RESULT 14
 US-09-845-667-21
 Sequence 21. Application US/09845667
 Patent No. US20020065221A1
 GENERAL INFORMATION:
 APPLICANT: Cohen, Philip
 Alessi, Dario
 Cross, Darren
 TITLE OF INVENTION: CONTROL OF PROTEIN SYNTHESIS, AND SCREENING METHOD
 FOR AGENTS
 NUMBER OF SEQUENCES: 58
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Braman & Rogalskyj, LLP
 STREET: P.O. Box 352
 CITY: Canandaigua
 STATE: New York
 COUNTRY: USA
 ZIP: 14424-0352
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/845.667
 FILING DATE: 30-Apr-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/091,763
 FILING DATE: 19-JUN-1998
 APPLICATION NUMBER: PCT/GB96/03186
 FILING DATE: 20-DEC-1996
 APPLICATION NUMBER: GB 9526083.2
 FILING DATE: 0-DEC-1995
 APPLICATION NUMBER: GB 9610272.8
 FILING DATE: 16-MAY-1996
 APPLICATION NUMBER: GB 9615066.9
 FILING DATE: 18-JUL-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Braman, Susan J
 REGISTRATION NUMBER: 34,103
 REFERENCE/DOCKET NUMBER: 002.00041
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 716-393-3002
 TELEFAX: 716-393-3001
 INFORMATION FOR SEQ ID NO: 21;
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Linear
 MOLECULE TYPE: Peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 56;
 US-09-845-667-56

Query Match 51.2%; Score 22; DB 9; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.2e+06;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 PRAAY 8
 Db 2 PRAATF 7

Db 2 PRAATE 7

Search completed: July 28, 2004, 08:00:13
Job time : 41 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 28, 2004, 07:52:54 ; Search time 18 Seconds
(without alignments)
22.945 Million cell updates/sec

Title: SEQ3
Perfect score: 43
Sequence: 1 qprraay 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 71086

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

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23: /cgns_6/podata/2/iaa/backfile1.pep:
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25: /cgns_6/podata/2/iaa/backfile1.pep:
26: /cgns_6/podata/2/iaa/backfile1.pep:
27: /cgns_6/podata/2/iaa/backfile1.pep:

RESULT 1
US-08-291-349A-5
; Sequence 5, Application US/08291349A
; Patent No. 5545620
; GENERAL INFORMATION:
; APPLICANT: Wahl, Sharon M.
; APPLICANT: McCarthy, James B.
; APPLICANT: Furth, Leo T.
; TITLE OF INVENTION: Synthetic Fibronectin Fragments As
; Inhibitors of Retroviral Infection
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff
; STREET: 10 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; SOFTWARE: Patent in Release #1.0, Version #1.25
; APPLICATION NUMBER: US/08/291,349A
; FILING DATE: 16 Aug 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/006,121
; FILING DATE: 19 JAN 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: McDonald, John J.
; REGISTRATION NUMBER: 26,949
; REFILE/DOCKET NUMBER: 92,673-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..8
; OTHER INFORMATION: /note= "EN5 (1892-1899)

Result No.	Score	Query Match Length	DB ID	Description
1	31	72.1	8 1 US-08-291-349A-5	Sequence 5, Appli
2	31	72.1	8 2 US-07-990-996-3	Sequence 3, Appli
3	31	72.1	8 2 US-08-480-133A-3	Sequence 2, Appli
4	31	72.1	8 2 US-08-99-965-2	Sequence 6, Appli
5	31	72.1	8 2 US-08-435-149-6	Sequence 10, Appli
6	31	72.1	8 2 US-09-02-706-10	Sequence 13, Appli
7	31	72.1	8 3 US-08-394-478A-10	Sequence 3, Appli
8	31	72.1	8 3 US-08-916-213A-3	Sequence 10, Appli
9	31	72.1	8 3 US-09-025-022-10	Sequence 11, Appli
10	31	72.1	8 3 US-08-04-165-11	Sequence 6, Appli
11	31	72.1	8 3 US-08-96-054A-6	Sequence 5, Appli
12	31	72.1	8 3 US-08-938-993A-6	Sequence 2, Appli
13	31	72.1	8 4 US-08-959-206A-2	Sequence 89, Appli
14	31	72.1	8 4 US-09-1704-170-89	Sequence 58, Appli
15	31	72.1	8 4 US-09-591-151A-38	Sequence 3, Appli
16	31	72.1	8 4 US-09-592-715-2	Sequence 13, Appli
17	31	72.1	8 5 PCT-US93-11781-3	Sequence 89, Appli
18	31	72.1	8 5 PCT-US95-02478-13	Sequence 7, Appli
19	28	65.1	6 1 US-08-704-170-89	Sequence 3, Appli
20	28	65.1	6 1 PCT-US94-07631-89	Sequence 89, Appli
21	28	65.1	7 1 US-08-127-499A-7	Sequence 7, Appli
22	28	65.1	7 1 US-08-482-847-7	Sequence 3, Appli
23	28	65.1	8 3 US-08-96-054A-3	Sequence 3, Appli
24	28	65.1	8 3 US-08-958-993A-3	Sequence 25, Appli
25	25	58.1	7 1 US-08-127-499A-25	Sequence 23, Appli
26	25	58.1	7 1 US-08-482-847-25	Sequence 3, Appli
27	24	55.8	7 1 US-08-127-499A-3	Sequence 3, Appli

OTHER INFORMATION: Fibronectin fragment : FN-C/H-V"

Query Match 72.1%; Score 31; DB 1; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 OPPRAAI 7
Db 2 QPPRARI 8

RESULT 2
US-07-990-296-3
Sequence 3, Application US/07990296
Patent No. 5591719

GENERAL INFORMATION:
APPLICANT: Furcht, Leo T.
ADDRESS: 90 South 7th Street, 3100 No. 5840691west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA

APPLICANT: Wahl, Sharon M.
ADDRESS: Merchant & Gould
CITY: Minneapolis
STATE: MN
COUNTRY: USA

APPLICANT: McCarthy, James B.
TITLE OF INVENTION: Method for Treating Acute and Chronic Inflammatory Disorders Using Polypeptides

NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
STREET: 3100 No. 5591719west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA

ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/990,296
FILING DATE: 1993/12/10
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kowalchyk, Alan W.
REGISTRATION NUMBER: 31,535
REFERENCE/DOCKET NUMBER: 600-252-US-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acid residues
TYPE: AMINO ACID
TOPOLOGY: Linear
MOLECULE TYPE: Peptide
FRAGMENT TYPE: Internal Fragment
ORIGINAL SOURCE: Synthetically Derived
FEATURE:
NAME/KEY: Fragment of the 33 kD carboxy terminal heparin-binding fragment of the A
NAME/KEY: chain of fibronectin
LOCATION: Represents isolated fibronectin
LOCATION: residues 1892-1899 from all plasma isoforms
LOCATION: of fibronectin

Query Match 72.1%; Score 31; DB 1; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 OPPRAAI 7
Db 2 QPPRARI 8

RESULT 3
US-08-480-133A-3
Sequence 3, Application US/08480133A
Patent No. 5840691
GENERAL INFORMATION:
APPLICANT: Furcht, Leo T.
APPLICANT: McCarthy, James B.
APPLICANT: Wahl, Sharon M.
APPLICANT: Allen, Janice B.
APPLICANT: Billups, Kevin L.
APPLICANT: Everett, Jeffrey B.
TITLE OF INVENTION: Method for Treating Inflammatory Diseases Using Polypeptides with Fibronectin Activity
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESS: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 5840691west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA

ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,133A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/139,903
FILING DATE: 21-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,296
FILING DATE: 10-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 600-308US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide

Query Match 72.1%; Score 31; DB 2; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 OPPRAAI 7
Db 2 QPPRARI 8

RESULT 4
US-08-480-133A-3
Sequence 2, Application US/08480133A
Patent No. 5833744
GENERAL INFORMATION:
APPLICANT: MODADIAN, DANIEL L.
APPLICANT: FIELDS, GREGG B.
TITLE OF INVENTION: METHOD FOR MODIFYING A SUBSTRATE SURFACE
TITLE OF INVENTION: TO INCLUDE A BIOMOLECULE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:

ADDRESSEE: MÜBTING, RASCH, GEBHARDT & SCHWAPPACH, P.A.
 STREET: 119 No. 5853/744th Fourth Street, Suite 203
 CITY: Minneapolis
 STATE: Minnesota
 ZIP: 55401

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/699,965
 FILING DATE: 20-AUG-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: MÜBTING, ANN M.
 REGISTRATION NUMBER: 33,977
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 612-305-1228
 TELEFAX: 612-305-1228

SEQUENCE FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

US-08-699-965-2

Query Match 72.1%; Score 31; DB 2; Length 8;
 Best Local Similarity 85.7%; Pred. No. 3e+05;
 Matches 6; Conservative 0; Mismatches 1; Indels 0;
 Gaps 0;

QY 1 QPPRAAI 7
 Db 2 QPPRAAI 8

RESULT 5
 Sequence 6, Application US/08435149
 Patent No. 5866402

GENERAL INFORMATION:
 APPLICANT: CREESEY, ABIA A.
 APPLICANT: INNIS, MICHAEL A.
 APPLICANT: ZAROR, ISABEL

TITLE OF INVENTION: CHIMERIC MCP AND DAP PROTEINS WITH CELL SURFACE LOCALIZING DOMAIN
 NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:
 ADDRESSEE: CHIRON CORPORATION
 STREET: INTELLECTUAL PROPERTY - R44C, P.O. BOX 8097
 CITY: EMERYVILLE
 STATE: CALIFORNIA
 ZIP: 94662-8097

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/435,149
 FILING DATE: 05-MAY-1995
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: SAVEREIDE, PAUL B.
 REGISTRATION NUMBER: 36,914
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (510) 601-2585

US-08-435-149-6

Query Match 72.1%; Score 31; DB 2; Length 8;
 Best Local Similarity 85.7%; Pred. No. 3e+05;
 Matches 6; Conservative 0; Mismatches 1; Indels 0;
 Gaps 0;

QY 1 QPPRAAI 7
 Db 2 QPPRAAI 8

RESULT 6
 US-09-025-706-10

Sequence 10, Application US/09025706
 Patent No. 5956874

GENERAL INFORMATION:
 APPLICANT: Clark, Richard A.
 APPLICANT: Greiling, Doris
 APPLICANT: Gailit, James

TITLE OF INVENTION: RECOMBINANT FIBRONECTIN-BASED EXTRACELLULAR MATRIX FOR WOUND HEALING

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jaekle Fleischmann & Mugel, LLP
 STREET: 39 State Street
 CITY: Roehampton
 STATE: New York
 COUNTRY: USA
 ZIP: 14614-1110

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/025,706
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Braman, Susan J.
 REGISTRATION NUMBER: 34,103
 REFERENCE/DOCKET NUMBER: 87653.97R263
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 716-262-31640
 TELEFAX: 716-262-4133
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide

US-09-025-706-10

Query Match 72.1%; Score 31; DB 2; Length 8;
 Best Local Similarity 85.7%; Pred. No. 3e+05;
 Matches 6; Conservative 0; Mismatches 1; Indels 0;
 Gaps 0;

QY 1 QPPRAAI 7
 Db 2 QPPRAAI 8

RESULT 7

US-08-394-748A-13
 / Sequence 13, Application US/08394748A
 / Patent No. 6013628
 / GENERAL INFORMATION:
 / APPLICANT: Skubitz, Amy P.N.
 / APPLICANT: Furth, Leo T.
 / APPLICANT: Baines, Mark
 / APPLICANT: Gregerson, Dale S.
 / APPLICANT: Agarwa, Anitc.
 / APPLICANT: Wright, Marsha M.
 / APPLICANT: Murali, Shobana
 / TITLE OF INVENTION: Method for Treating Conditions of the Eye
 / NUMBER OF SEQUENCES: 16
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Merchant & Gould
 / STREET: 3100 No. 6013628West Center
 / CITY: Minneapolis
 / STATE: MN
 / COUNTRY: USA
 / ZIP: 55402
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: PatentIn Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/394,748A
 / FILING DATE: 27-FEB-1995
 / CLASSIFICATION:
 / PRIORITY APPLICATION DATA:
 / APPLICATION NUMBER: US 08/203,458
 / FILING DATE: 28-FEB-1994
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Carter, Charles G.
 / REGISTRATION NUMBER: 35,033
 / REFERENCE/DOCKET NUMBER: 600.307US01
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 612-332-5300
 / TELEFAX: 612-332-9081
 / INFORMATION FOR SEQ ID NO: 13:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 8 amino acids
 / TYPE: amino acid
 / TOPOLOGY: linear
 / MOLECULE TYPE: peptide
 / ORIGINAL SOURCE:
 / STRAIN: FN-C/H-V
 / US-08-394-748A-13

Query Match 72.1%; Score 31; DB 3; Length 8;
 Best Local Similarity 85.7%; Pred. No. 3e+05; 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 1; Indels 0;

Qy 1 QPPRARI 7
 Db 2 QPPRARI 8

RESULT 9
 US-09-025-622-10
 / Sequence 10, Application US/09025622
 / Parent No. 6194378
 / GENERAL INFORMATION:
 / APPLICANT: Clark, Richard A.
 / APPLICANT: Greiling, Doris
 / TITLE OF INVENTION: FIBRONECTIN PEPTIDES-BASED EXTRACELLULAR
 / NUMBER OF SEQUENCES: 12
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Jaekle Fleischmann & Mugel, LLP
 / STREET: 39 State Street
 / CITY: Rochester
 / STATE: New York
 / COUNTRY: USA
 / ZIP: 14614-3310
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: PatentIn Release #1.0, Version #1.30
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/09/025,622
 / FILING DATE:
 / CLASSIFICATION:
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Braman, Susan J.
 / REGISTRATION NUMBER: 34,103
 / REFERENCE/DOCKET NUMBER: 87653.97R270
 / TELECOMMUNICATION INFORMATION:

RESULT 8
 US-08-916-913A-3
 / Sequence 3, Application US/08916913A
 / Patent No. 6121027
 / GENERAL INFORMATION:
 / APPLICANT: Clapper, David L.
 / APPLICANT: Swanson, Melvin J.
 / APPLICANT: Hu, Sheu-Ping
 / APPLICANT: Amos, Richard A.
 / APPLICANT: Eversen, Terrence P.
 / TITLE OF INVENTION: LATENT REACTIVE POLYMERS WITH
 / NUMBER OF SEQUENCES: 16
 / CORRESPONDENCE ADDRESS:

```

Db 2 QPPRARI 8

; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-025-622-10

Query Match 72.1%; Score 31; DB 3; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 1; Software: Patent in Ver. 2.1
Qy 1 QPPRARI 7
Db 2 QPPRARI 8

RESULT 10
US-08-847-065-11
; Sequence 11, Application US/08847065
; Patent No. 6245335
; GENERAL INFORMATION:
; APPLICANT: Masure, H. Robert
; APPLICANT: Rosenow, Carsten I.
; APPLICANT: Tuominen, Elmera M.
; TITLE OF INVENTION: CHOLINE BINDING PROTEINS FOR
; NUMBER OF SEQUENCES: 25
; TITLE OF INVENTION: ANTI-PNEUMOCOCCAL VACCINES
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/847,065
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-158 ..
; TELEPHONE: 201-437-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-847-065-11

Query Match 72.1%; Score 31; DB 3; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 1; Software: Patent in Ver. 2.1
Qy 1 QPPRARI 7
Db 2 QPPRARI 8

RESULT 11
US-08-960-054A-6
; Sequence 6, Application US/08860054A
; Patent No. 6261537
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to
; TITLE OF INVENTION: diagnostic/therapeutic
; FILE REFERENCE: REF/Klaveness/054
; CURRENT APPLICATION NUMBER: US/08/960,054A
; CURRENT FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO: 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; Sequence: Fibronectin
; OTHER INFORMATION: Sequence: Fibronectin
; OTHER INFORMATION: Peptide
; US-08-960-054A-6

Query Match 72.1%; Score 31; DB 3; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 1; Software: Patent in Ver. 2.1
Qy 1 QPPRARI 7
Db 2 QPPRARI 8

RESULT 12
US-08-258-993A-6
; Sequence 6, Application US/08958993A
; Patent No. 6269117
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
; TITLE OF INVENTION: agents
; FILE REFERENCE: REF/Klaveness/993
; CURRENT APPLICATION NUMBER: US/08/958,993A
; CURRENT FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO: 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Peptide
; US-08-258-993A-6

Query Match 72.1%; Score 31; DB 3; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 1; Software: Patent in Ver. 2.1
Qy 1 QPPRARI 7
Db 2 QPPRARI 8

RESULT 13
US-08-959-206A-2
; Sequence 2, Application US/08959206A
; Patent No. 631289
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Fibronectin
; FILE REFERENCE: REF/Klaveness/2
; CURRENT APPLICATION NUMBER: US/08/959206A
; CURRENT FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO: 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fibronectin
; US-08-959-206A-2

Query Match 72.1%; Score 31; DB 3; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 1; Software: Patent in Ver. 2.1
Qy 1 QPPRARI 7
Db 2 QPPRARI 8

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1 TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
 1
 1 TITLE OF INVENTION: agents
 1 FILE REFERENCE: RE/P/Klaviness/206
 1 CURRENT APPLICATION NUMBER: US/08/959,206A
 1 CURRENT FILING DATE: 1997-10-24
 1 NUMBER OF SEQ ID NOS: 27
 1 SOFTWARE: PatentIn Ver. 2.1
 1 LENGTH: 8
 1 TYPE: PRT
 1 ORGANISM: Artificial Sequence
 1 FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Fibronectin
 1
 1 OTHER INFORMATION: Description of Artificial Sequence: Fibronectin
 1 US-08/959-206A-2

Query Match	72.1%	Score 31;	DB 4;	Length 8;
Best Local Similarity	85.7%	Pred. No.	3e+05;	
Matches	6;	Mismatches	1;	Indels 0;
Db	1 OPPRAAI 7			
	2 OPPRARI 8			

RESULT 14
 US-09-101-751A-58
 1 Sequence 58, Application US/09101751A
 1 Patent No. 6,645,253
 1 GENERAL INFORMATION:
 1 APPLICANT: WICKHAM, THOMAS J.
 1 APPLICANT: KOVSEDI, IMRE
 1 APPLICANT: BROUCH, DOUGLAS E.
 1 TITLE OF INVENTION: VECTORS AND METHODS FOR GENE TRANSFER TO CELLS
 1 FILE REFERENCE: 85710
 1 CURRENT APPLICATION NUMBER: US/09/101,751A
 1 CURRENT FILING DATE: 1999-01-29
 1 PRIOR APPLICATION NUMBER: WO 96US19150
 1 PRIOR FILING DATE: 1996-11-27
 1 PRIOR APPLICATION NUMBER: US 08/700,846
 1 PRIOR FILING DATE: 1995-08-21
 1 PRIOR APPLICATION NUMBER: US 08/563,368
 1 PRIOR FILING DATE: 1995-11-28
 1 NUMBER OF SEQ ID NOS: 94
 1 SOFTWARE: PatentIn Ver. 2.1
 1 LENGTH: 8
 1 TYPE: PRT
 1 ORGANISM: Unknown Organism
 1 FEATURE: misc. feature
 1 LOCATION: () .()
 1 OTHER INFORMATION: Description of Unknown Organism: Artificial
 1 US-09-101-751A-58

Query Match	72.1%	Score 31;	DB 4;	Length 8;
Best Local Similarity	85.7%	Pred. No.	3e+05;	
Matches	6;	Mismatches	0;	Indels 1;
Db	1 OPPRAAI 7			
	2 OPPRARI 8			

Search completed: July 28, 2004, 07:55:51
 Job time : 18 secs

RESULT 15
 US-09-591-564-3
 1 Sequence 3, Application US/09591564
 1 Patent No. 6,147,34
 1 GENERAL INFORMATION:
 1 APPLICANT: Clapper, David L.